Claims:

1. A method of quantitatively detecting genetically modified DNA (transgene) in foodstuffs,
characterized in that
the detection is performed using fluorescence-coupled PCR, said method involving extracting the total DNA from the food sample, and
   a) determining the amount of transgene in the total DNA by performing a PCR reaction with a transgene-specific fluorescence-labelled probe S1 and two transgene-specific primers P1 and P2 in a first reaction vessel and measuring the change in fluorescence radiation as compared to a control, a synthetic gene fragment (target IAC DNA) in addition to the primers P1 and P2 and a fluorescence-labelled probe S2 being used as internal amplification control (IAC) for transgene determination in the first reaction vessel, which fragment has two binding sites for the primers P1 and P2 and one binding site for the fluorescence-labelled probe S2 which not only differs from probe S1 in its sequence but also is labelled with a fluorescent dye other than that of probe S1;
   b) selecting a reference gene and determining the amount of reference gene in the total DNA by performing a PCR reaction with a reference gene-specific fluorescence-labelled probe S3 and two reference gene-specific primers P3 and P4 in a second reaction vessel and measuring the change in fluorescence radiation as compared to a control, a synthetic gene fragment (reference IAC DNA) in addition to the primers P3 and

P4 and the fluorescence-labelled probe S2 being used as internal amplification control (IAC) for reference gene determination in the second reaction vessel, which fragment has two binding sites for the primers P3 and P4 and one binding site for the fluorescence-labelled probe S2 which is identical to the fluorescence-labelled probe S2 in the target gene system, but differs from probe S3 with respect to sequence and fluorescent dye; and

ultimately, calculating the level of genetically modified DNA from the ratio of the amounts of transgene and reference gene.

2. The method according to claim 1, wherein the Roundup Ready soy gene (RRS gene) is detected as transgene.

3. The method according to claim 1, wherein the nucleic acid sequence SEQ ID NO. 2 or SEQ ID NO. 2a or variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as probe S1.

4. The method according to claim 1, wherein the nucleic acid sequence SEQ ID NO. 3 or SEQ ID NO. 3a and the nucleic acid sequence SEQ ID NO. 4 or SEQ ID NO. 4a or the variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as primer P1 and primer P2, respectively.

5. The method according to claim 1, wherein the lectin gene having the SEQ ID No. 11 is used as reference gene.

6. The method according to claim 1, wherein the nucleic acid sequence SEQ ID NO. 5 or variants thereof obtained by de-

letion, substitution or addition and having at least 80% homology are used as probe S3.

7. The method according to claim 1, wherein the NA sequence SEQ ID NO. 6 or SEQ ID NO. 6a and the NA sequence SEQ ID NO. 7 or the variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as primer P3 and primer P4, respectively.

8. The method according to claim 1, wherein the NA sequence SEQ ID NO. 8 or SEQ ID NO. 8a or variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as synthetic gene fragment of the internal amplification control for transgene determination (target IAC DNA).

9. The method according to claim 1, wherein the NA sequence SEQ ID NO. 10 or SEQ ID NO. 10a or variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as synthetic gene fragment of the internal amplification control for reference gene determination (reference IAC DNA).

10. The method according to claim 1, wherein the Bt-176 maize gene is detected as transgene.

11. The method according to claim 1, wherein the sequence SEQ ID NO. 12 or variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as probe S1.

12. The method according to claim 1, wherein the sequence SEQ ID NO. 13 and the sequence SEQ ID NO. 14 or variants thereof obtained by deletion, substitution or addition

and having at least 80% homology are used as primer P1 and primer P2, respectively.

13. The method according to claim 1, wherein the invertase gene of maize is used as reference gene.

14. The method according to claim 1, wherein the sequence SEQ ID NO. 15 or variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as probe S3.

15. The method according to claim 1, wherein that the sequence SEQ ID NO. 16 and the sequence SEQ ID NO. 17 or variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as primer P3 and primer P4, respectively.

16. The method according to claim 1, wherein the sequence SEQ ID NO. 18 or variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as target IAC DNA.

17. The method according to claim 1, wherein the sequence SEQ ID NO. 19 or variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as reference IAC DNA.

18. The method according to claim 1, wherein the nucleic acid sequence SEQ ID NO. 9 or variants thereof obtained by deletion, substitution or addition and having at least 80% homology are used as probe S2.

19. The method according to claim 18, wherein the probe S2 at its 5' end or its 3' end is labelled with a reporter

fluorescent dye, preferably a fluorescein derivative selected from 6-carboxyfluorescein, tetrachloro-6-carboxyfluorescein, 2,7-dimethoxy-4,5-dichloro-6-carboxyfluorescein, hexachloro-6-carboxyfluorescein, which dye is different from that of probes S1 and S3, and at its other sequence end, the probe S2 is labelled with a quencher, preferably a rhodamine derivative identical to that of probes S1 and S3, preferably with TAMRA.

20. The method according to claim 1, wherein the probes S1 and S3 are labelled at their 5' end or at their 3' end with a reporter fluorescent dye, preferably a fluorescein derivative selected from 6-carboxyfluorescein, tetrachloro-6-carboxyfluorescein, 2,7-dimethoxy-4,5-dichloro-6-carboxyfluorescein, hexachloro-6-carboxyfluorescein, preferably with 6-carboxyfluorescein (FAM), and at each of their other ends with a quencher, preferably a rhodamine derivative, preferably with 6-carboxy-tetramethylrhodamine (TAMRA).

21. A test kit for the quantitative detection of genetically modified DNA (transgene) in foods using fluorescence-coupled PCR, comprising a transgene-specific, fluorescence-labelled probe S1 and two transgene-specific primers P1 and P2, a reference gene-specific, fluorescence-labelled probe S3, and two reference gene-specific primers P3 and P4, as well as a fluorescence-labelled probe S2 as internal amplification control, which probe differs from probes S1 and S3 both in its sequence and its fluorescence-labelling, a synthetic gene fragment (target IAC DNA) having two binding sites for the primers P1 and P2 and one binding site for the probe S2, and a synthetic gene fragment (reference IAC DNA) having two binding

sites for the primers P3 and P4 and one binding site for the probe S2.

22. The test kit according to claim 21, used in the detection of the RRS gene.

23. The test kit according to claim 21, used in the detection of the Bt-176 maize gene.

24. The test kit according to claim 21, wherein the kit includes as probe S2 the sequence SEQ ID NO. 9 or variants thereof having at least 80% homology.